

Please replace the third full paragraph on page 13 (lines 26-33) with the following paragraph re-written in clean form:

In another preferred embodiment, one or more insertions are present in the VP3 structural protein (Rutledge, E.A. et al. (1998) supra) before and/or after at least one amino acid in the sequence selected from YKQIS SQSGA (SEQ ID NO: 2), YLTLN NGSQA (SEQ ID NO: 3), YYLSR TNTPS (SEQ ID NO: 4), EEKFF PQSGV (SEQ ID NO: 5), NPVAT (SEQ ID NO: 6), EQYGS (SEQ ID NO: 7), LQRGN RQAAT (SEQ ID NO: 8), NVDFVTDTNG (SEQ ID NO: 9), because these sites are located on the exposed sites of a loop, in which case the risk of altering the VP3 structure is small.

Please replace the second full paragraph on page 17 (lines 15-23) with the following paragraph re-written in clean form:

#### Mutations in VP3

- |    |                     |                 |
|----|---------------------|-----------------|
| a) | ins261; YKQIS SQSGA | (SEQ ID NO: 10) |
| b) | ins381; YLTLN NGSQA | (SEQ ID NO: 11) |
| c) | ins447; YYLSR TNTPS | (SEQ ID NO: 12) |
| d) | ins534; EEKFF PQSGV | (SEQ ID NO: 13) |
| e) | ins573; NPVAT EQYGS | (SEQ ID NO: 14) |
| f) | ins587; LQRGN RQAAT | (SEQ ID NO: 15) |
| g) | ins713; NVDFVTDTNG  | (SEQ ID NO: 16) |

Please replace the third partial paragraph on page 22 (lines 26-39) and the first partial paragraph on page 23 (lines 1-8) with the following paragraph re-written in clean form:

This shows that insertion of the QAGTFALRGDNPQG (SEQ ID NO: 1) peptide alters the elution behavior of the AAV particles so that, at the same pH, the mutated particles elute at a lower salt concentration than the wild-type particles. This means that the virus fraction is shifted toward other fractions which are in some circumstances less impure or otherwise more suitable. It is therefore possible to alter the chromatographic properties of the AAV particles by insertions, deletions or other modifications of the capsid proteins. It is possible in particular in one variant of the invention shown to construct, by introducing amino acids with a predominantly positive charge, for example at the insertion sites shown in the examples, capsid mutants of the invention which elute at higher salt concentrations compared with the wild type (which elutes in a broad, less impure peak).